

FIG. 1

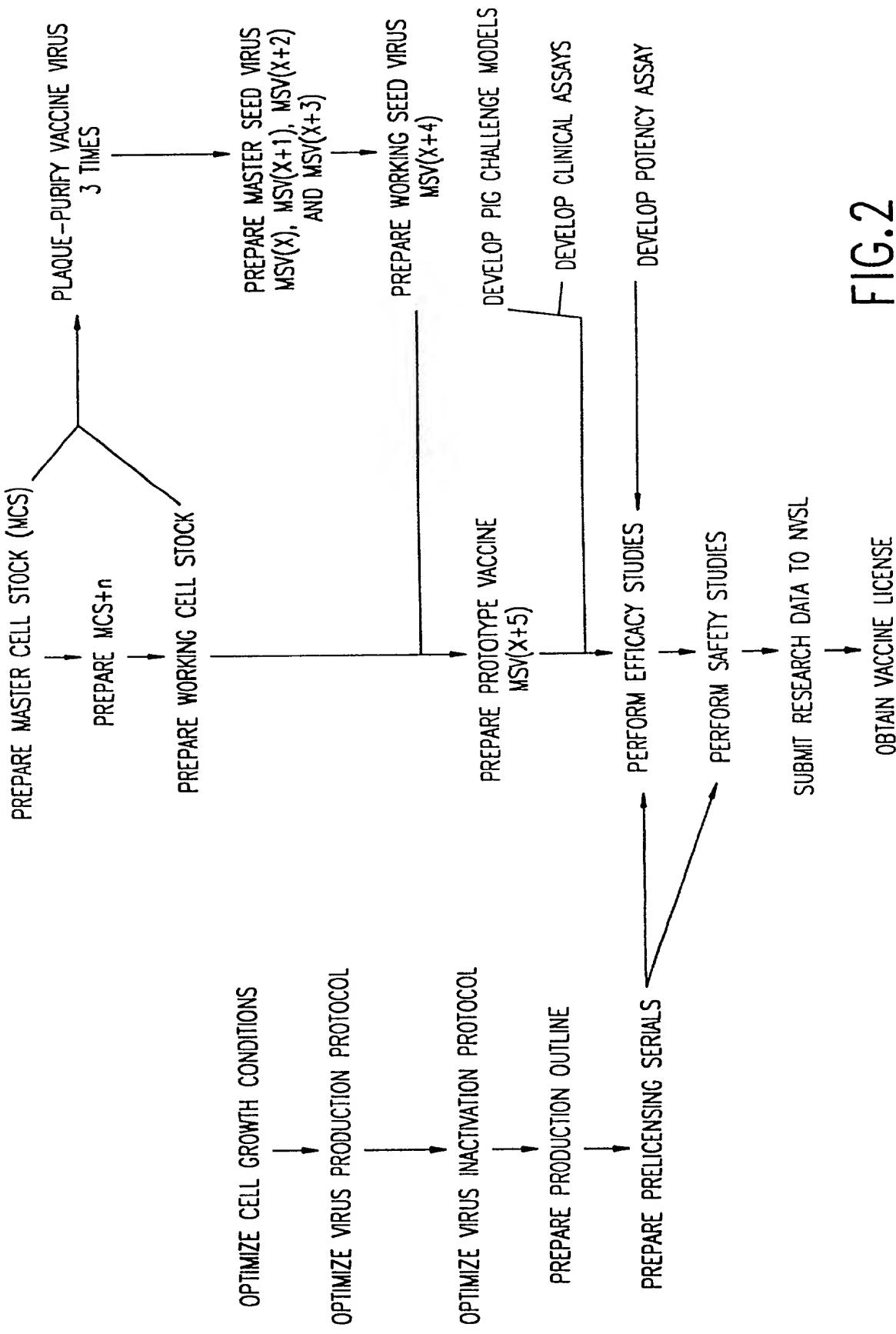


FIG. 2

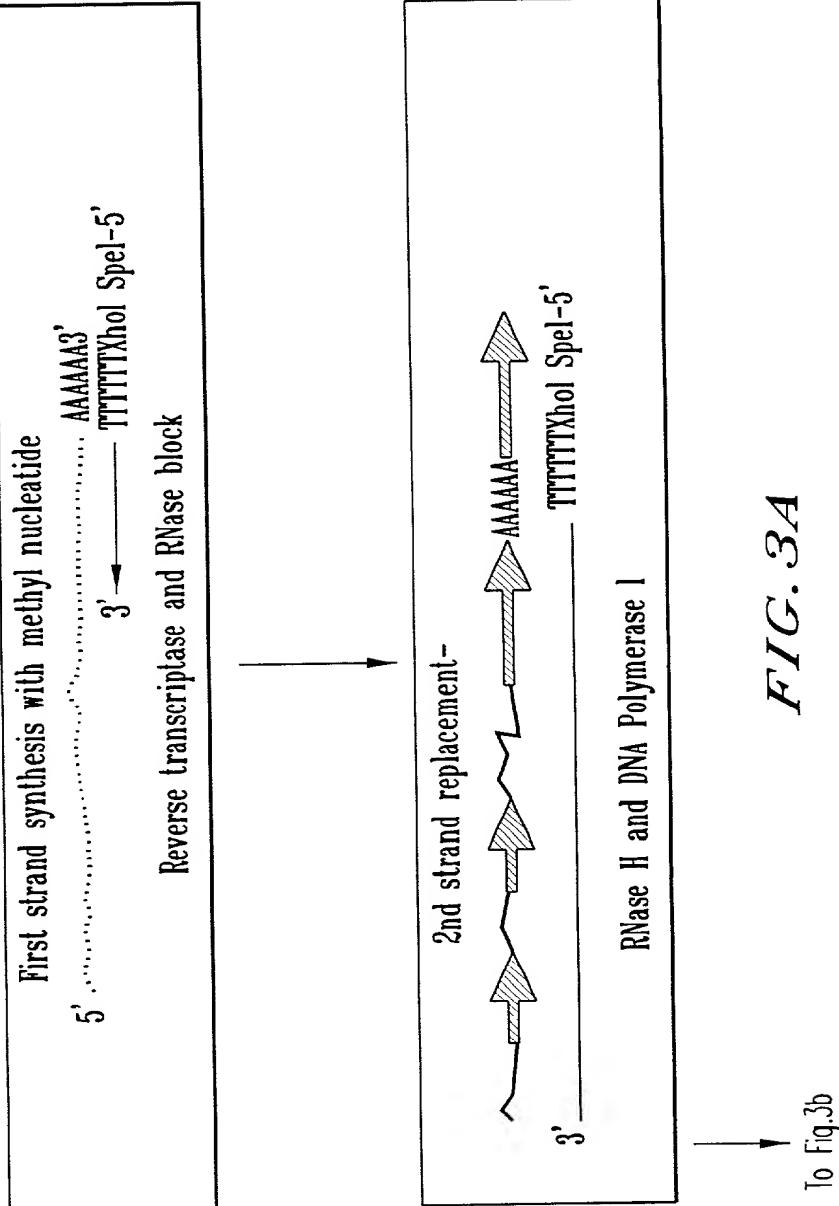


FIG. 3A

To Fig. 3b

From Fig.3a

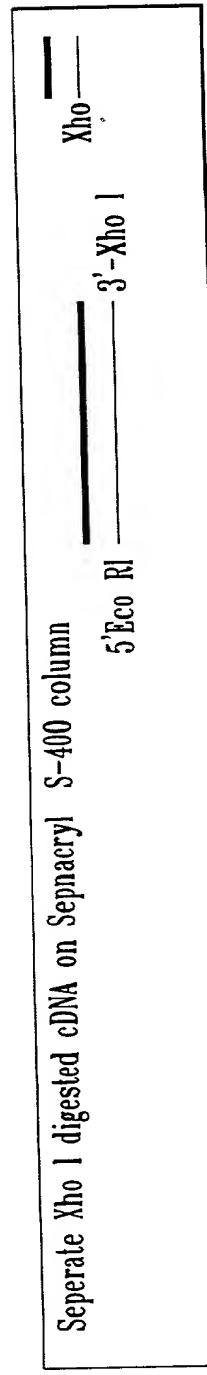
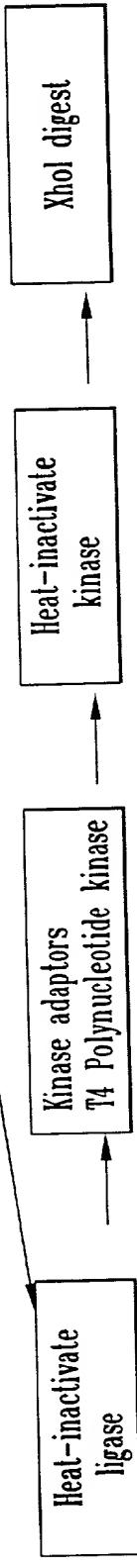
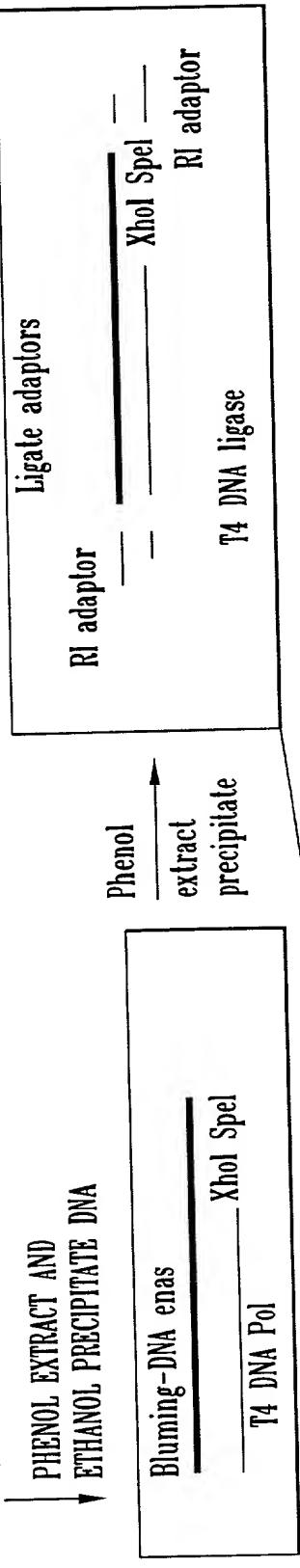
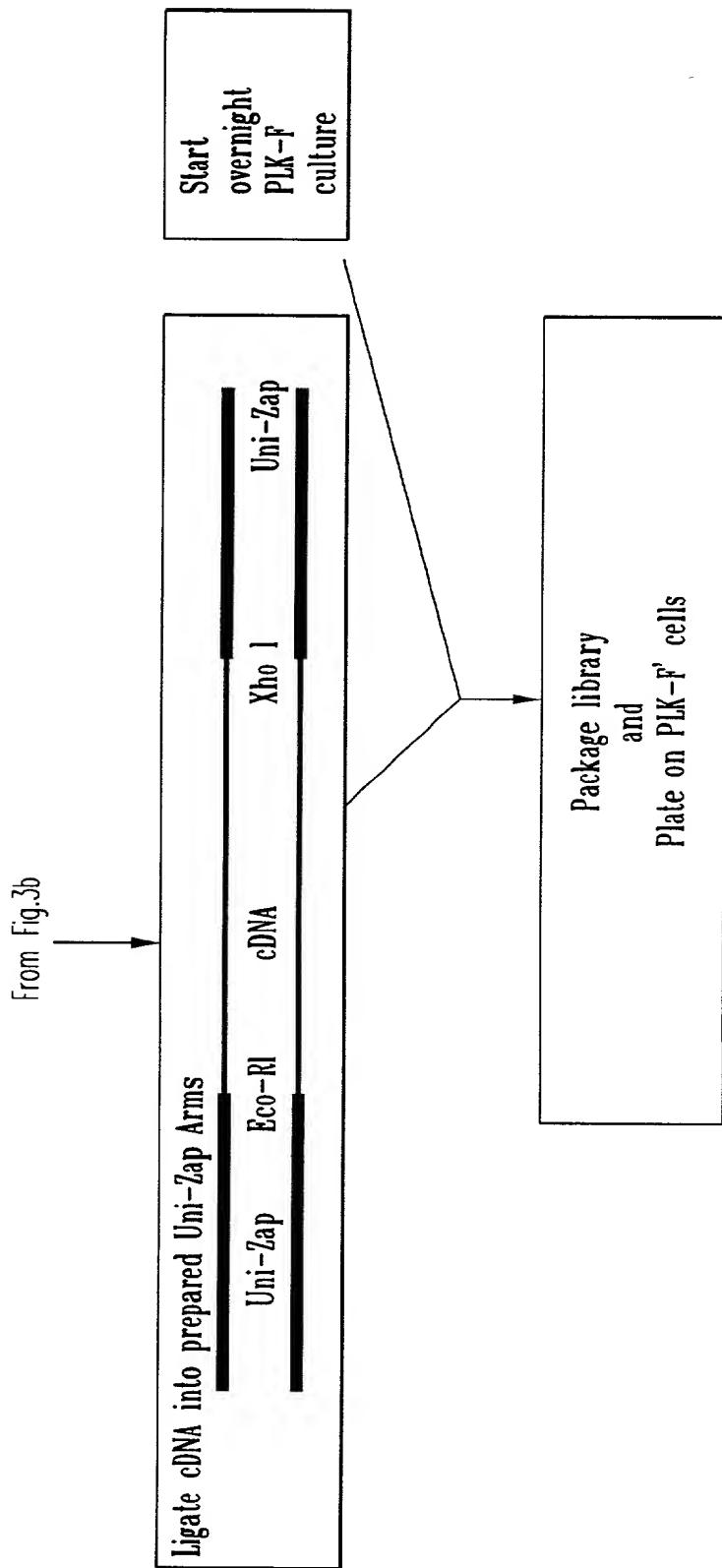


FIG. 3B

To Fig.3c

*FIG. 3c*



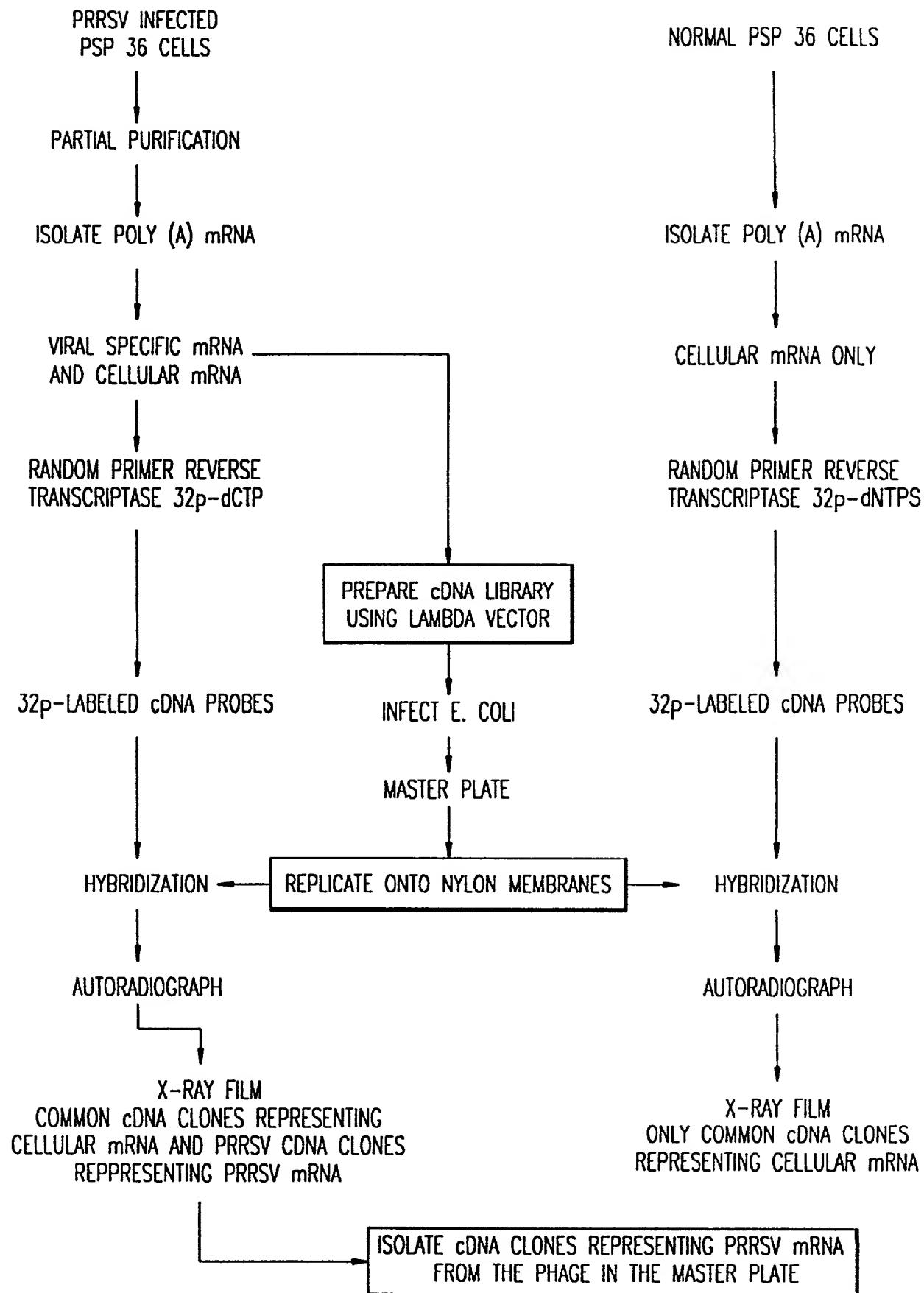
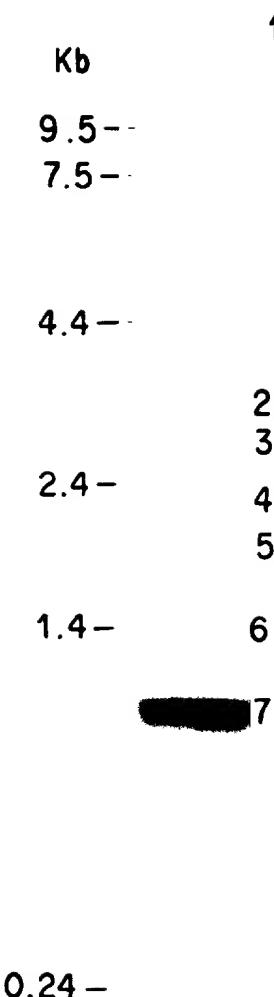
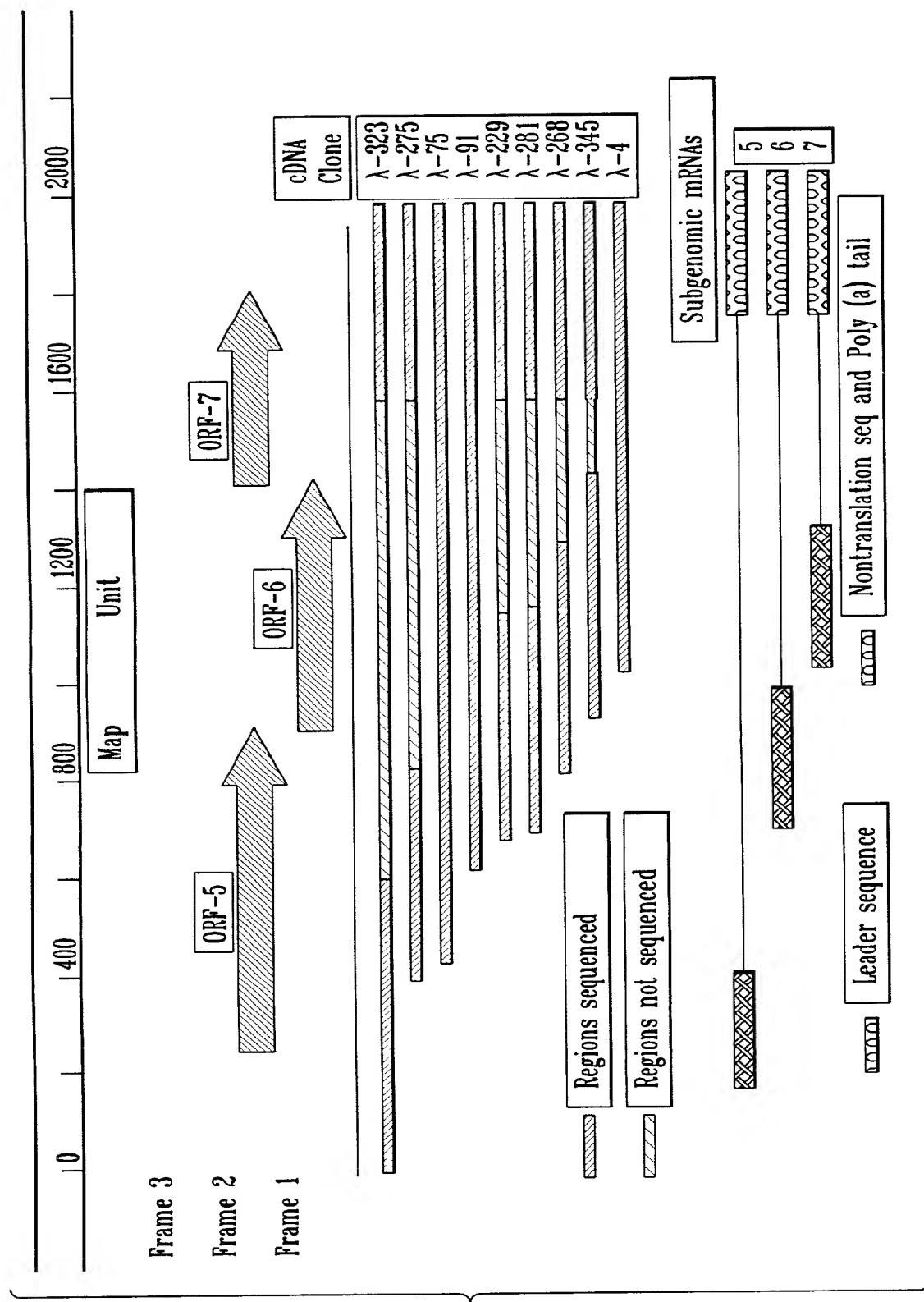


FIG.4



**FIG. 5**

*FIG. 6*



GGCAAGGCTTGGCTGCCTCCAAGACATCAGTTGGCATCGCAACTCGGCCCTTGAGGGATTCCGAAAGTCCCCTAGTGGCACGGGAATGGG 100  
 ACACCCGTGATA[CACTG]CACAGGCAA[TGT]TACCGAT[GAGAA]TTATT[GCAATTCCCTGATCCTCTGATCTGTTCTCTGCTTCTGCTG 200  
 AGA[TGAGTGA]AAAGGGATTAAAGG[GGATTGGCAATGTTGGCAATGTTGGCATCGTGGCATGTCGCTCAACTTCACCAAGTTACGTCCAAACATGTCAAAGGAATT 300  
 TACCCAAACGTTCCCTGGTAGTTGACCATGTTGGGGCTGCTCATTTCATGACGCCCGAGACCATGAGGGGGCAACTGTTTAGCCCTGCTTTTGGCATT 400  
 DRF 4 stop  
 \*\*\* +1>DRF 5 start  
CTGTTGGCAATTTGAATGTTAAGTATGTTGGGAAAATGCTGGGAAATGCTTGGCCGGGCTGTTGGCTCGCAAATGCTTGGGTTGATCTGGCTGGGTCTTGGTTT 500  
 GTTGGGCTCGTCAGGGCAACGGGAACAGGGCAAGGGCTCAAATTTACAGCTGATTACAACCTGACGGCTATGTTGACCTGAAATGGCACAGATGGCTAGGCTAAATA 600  
 AATTGACTGGGAGTGGAGTGTTTGCACTACAATGTCCTTATGGTGCCTCACTACTAGCCATTTCCTTGACACAGTCGG 700  
 TCTGGTCACTGGCTACCGCTGGGTTGTCACGGGGGATGTTGAGTAGGATGTTGAGTGGCTGGCTGGCTGGGTGAGTTGGCTTCGTCATT 800  
 AGGCCTGGGAAGAA[TGGATGCTTGCTGGGCTACCTCACTGAACTAATACCAACTTCTCTGGACACTAAGGGAGACTCTATCGTGGGGTGGCTG 900  
 TCA[TCAAGAGAAAGGAAAGTTGAGGTCGAAGGTCACCTGATCAACCTCAAAAGAGTTGGCTTGA[TGGTTCCGGGCTACCCCCGTAACCAAGAGT 1000  
 DRF 6 start  
 +1> \*\*\*DRF 5 stop  
TTCAGGGAAACAATGGAGTCGTCCTTAGATGACTCTGTCATGATAGCAAGGCTCCACAAAAGGTCCTGGGTTTCTATTACCTACACGGCAGTGA 1100

*FIG. 7A*

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FIG. 7B

FIG. 8

Year	Deaths	Rate per 100,000	Rate per 100,000 in U.S.
1950	1,000	10.0	10.0
1951	1,000	10.0	10.0
1952	1,000	10.0	10.0
1953	1,000	10.0	10.0
1954	1,000	10.0	10.0
1955	1,000	10.0	10.0
1956	1,000	10.0	10.0
1957	1,000	10.0	10.0
1958	1,000	10.0	10.0
1959	1,000	10.0	10.0
1960	1,000	10.0	10.0
1961	1,000	10.0	10.0
1962	1,000	10.0	10.0
1963	1,000	10.0	10.0
1964	1,000	10.0	10.0
1965	1,000	10.0	10.0
1966	1,000	10.0	10.0
1967	1,000	10.0	10.0
1968	1,000	10.0	10.0
1969	1,000	10.0	10.0
1970	1,000	10.0	10.0
1971	1,000	10.0	10.0
1972	1,000	10.0	10.0
1973	1,000	10.0	10.0
1974	1,000	10.0	10.0
1975	1,000	10.0	10.0
1976	1,000	10.0	10.0
1977	1,000	10.0	10.0
1978	1,000	10.0	10.0
1979	1,000	10.0	10.0
1980	1,000	10.0	10.0
1981	1,000	10.0	10.0
1982	1,000	10.0	10.0
1983	1,000	10.0	10.0
1984	1,000	10.0	10.0
1985	1,000	10.0	10.0
1986	1,000	10.0	10.0
1987	1,000	10.0	10.0
1988	1,000	10.0	10.0
1989	1,000	10.0	10.0
1990	1,000	10.0	10.0
1991	1,000	10.0	10.0
1992	1,000	10.0	10.0
1993	1,000	10.0	10.0
1994	1,000	10.0	10.0
1995	1,000	10.0	10.0
1996	1,000	10.0	10.0
1997	1,000	10.0	10.0
1998	1,000	10.0	10.0
1999	1,000	10.0	10.0
2000	1,000	10.0	10.0
2001	1,000	10.0	10.0
2002	1,000	10.0	10.0
2003	1,000	10.0	10.0
2004	1,000	10.0	10.0
2005	1,000	10.0	10.0
2006	1,000	10.0	10.0
2007	1,000	10.0	10.0
2008	1,000	10.0	10.0
2009	1,000	10.0	10.0
2010	1,000	10.0	10.0
2011	1,000	10.0	10.0
2012	1,000	10.0	10.0
2013	1,000	10.0	10.0
2014	1,000	10.0	10.0
2015	1,000	10.0	10.0
2016	1,000	10.0	10.0
2017	1,000	10.0	10.0
2018	1,000	10.0	10.0
2019	1,000	10.0	10.0
2020	1,000	10.0	10.0
2021	1,000	10.0	10.0
2022	1,000	10.0	10.0
2023	1,000	10.0	10.0
2024	1,000	10.0	10.0
2025	1,000	10.0	10.0
2026	1,000	10.0	10.0
2027	1,000	10.0	10.0
2028	1,000	10.0	10.0
2029	1,000	10.0	10.0
2030	1,000	10.0	10.0
2031	1,000	10.0	10.0
2032	1,000	10.0	10.0
2033	1,000	10.0	10.0
2034	1,000	10.0	10.0
2035	1,000	10.0	10.0
2036	1,000	10.0	10.0
2037	1,000	10.0	10.0
2038	1,000	10.0	10.0
2039	1,000	10.0	10.0
2040	1,000	10.0	10.0
2041	1,000	10.0	10.0
2042	1,000	10.0	10.0
2043	1,000	10.0	10.0
2044	1,000	10.0	10.0
2045	1,000	10.0	10.0
2046	1,000	10.0	10.0
2047	1,000	10.0	10.0
2048	1,000	10.0	10.0
2049	1,000	10.0	10.0
2050	1,000	10.0	10.0
2051	1,000	10.0	10.0
2052	1,000	10.0	10.0
2053	1,000	10.0	10.0
2054	1,000	10.0	10.0
2055	1,000	10.0	10.0
2056	1,000	10.0	10.0
2057	1,000	10.0	10.0
2058	1,000	10.0	10.0
2059	1,000	10.0	10.0
2060	1,000	10.0	10.0
2061	1,000	10.0	10.0
2062	1,000	10.0	10.0
2063	1,000	10.0	10.0
2064	1,000	10.0	10.0
2065	1,000	10.0	10.0
2066	1,000	10.0	10.0
2067	1,000	10.0	10.0
2068	1,000	10.0	10.0
2069	1,000	10.0	10.0
2070	1,000	10.0	10.0
2071	1,000	10.0	10.0
2072	1,000	10.0	10.0
2073	1,000	10.0	10.0
2074	1,000	10.0	10.0
2075	1,000	10.0	10.0
2076	1,000	10.0	10.0
2077	1,000	10.0	10.0
2078	1,000	10.0	10.0
2079	1,000	10.0	10.0
2080	1,000	10.0	10.0
2081	1,000	10.0	10.0
2082	1,000	10.0	10.0
2083	1,000	10.0	10.0
2084	1,000	10.0	10.0
2085	1,000	10.0	10.0
2086	1,000	10.0	10.0
2087	1,000	10.0	10.0
2088	1,000	10.0	10.0
2089	1,000	10.0	10.0
2090	1,000	10.0	10.0
2091	1,000	10.0	10.0
2092	1,000	10.0	10.0
2093	1,000	10.0	10.0
2094	1,000	10.0	10.0
2095	1,000	10.0	10.0
2096	1,000	10.0	10.0
2097	1,000	10.0	10.0
2098	1,000	10.0	10.0
2099	1,000	10.0	10.0
2100	1,000	10.0	10.0

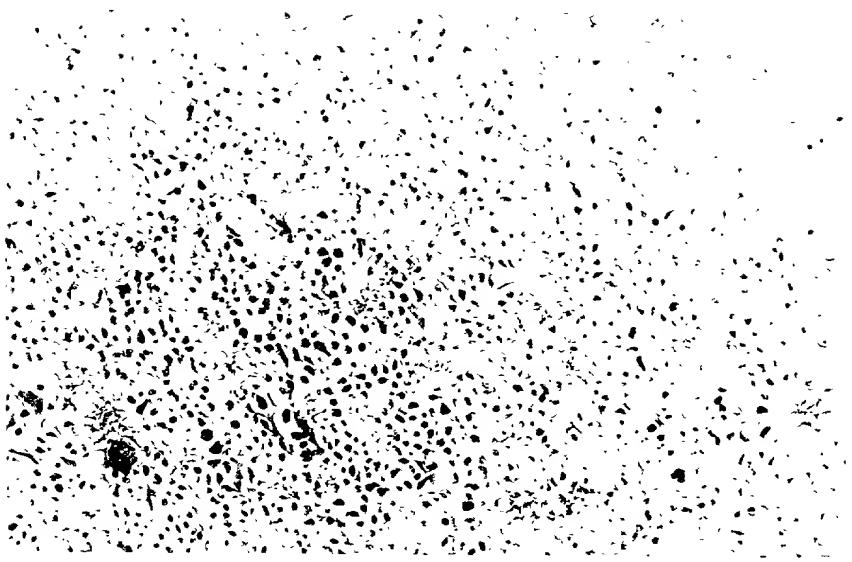
FIG. 9

Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	ATGGCCGTAA -.....-AT	AAAACCGA- -.....-AT	AAGAAAGT -.....-AT	A-CAG-----C ACAGAAAGAG	14632 1434	
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	TCGGA AAAGA	GGG GGGS	AATGCCAGC GATGCCAGC	CAGTCAATCA CAGTCAATCA	TCTGGGTG ATCTGGCT-	14681 1483
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	CAA -AA-	CTCC CAT	CTCCAGGC GGTCAAGAA	CTGGAACTTA AACCAGCTCA	TCTGGGTG ACGGG...-GA	14728 1528
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	AAGAAAAA -AA-	-G -G	-CTTGAGAAG CCGGAGAAG	CTGAGAAG CCCCATTCC	CCCTGGCTG CTCTACCGAC	14766 1578
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	TGAAAGT TGAAGATG	GAC ATG	ATGGCACC GTGAGACATC	ACTGCAACCA AGTTTACCC	TCCGTTGCT TAGTGCGT	14816 1628
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	TGCAA TGTCG	CGAT CGAT	CCAGAOGT CCAGAOGC	TTCAATCAAG TTTAATCAAG	TGCGTTGCT GGCGGGCAO	14865 1677
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	TTCAT GTCAG	TCCAGCTCA GGGAGTTAA	CTTTTCAGCT GTTAACACTG	TGAGTTAATG CGAGTTTACT	TGGCTGGCT TGGCAAG-C	14915 1727
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	GT GTCATA	CGGAACTTCA CAGTCAAGT	CTTTTCAGCT GGGCTGATTC	CTGGCGCTTG CTACACATTT	TGGCTGGCT TGGCAAG-C	14965 1774
Leystad seq (14588 - 14974) ISU 12/70/3' terminal (1403 - 1774)	GT ATCATA	GGCCCTGATT ATCATACTGT	GGGTGAACTT GGGCTGATTC	CTACACATGGC GATCAACGCT	CAGTCAGGGT CAG-GCATGAG-	14974 1774

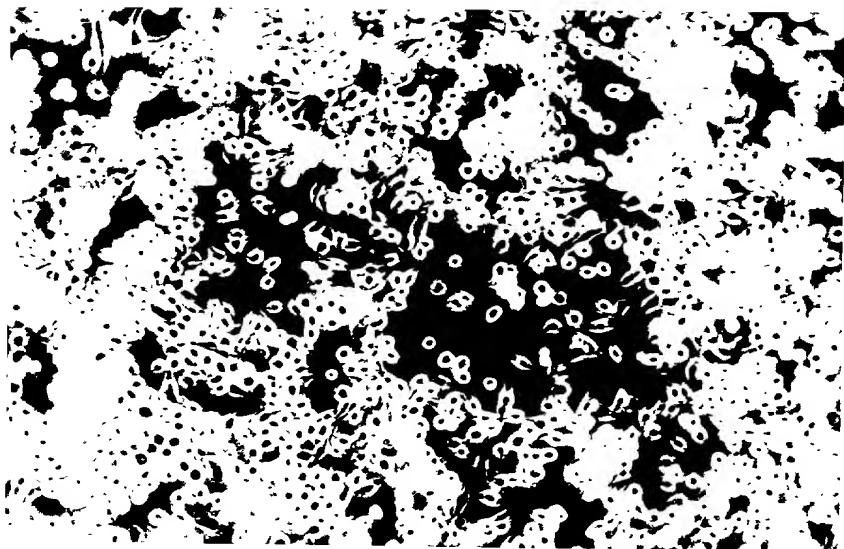
FIG. 10

ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	TGGCTGGCA TTCTTGAGGC ATCCCAGTGT TTGAATTGCA .....	1814 14976
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AGAA[TGCC]G GTGAAATGCCA C[TGAT]TGADA [TTTC]GCCTCT TGACAG[TCAG] G TGAATGGCC GCGATT[GCG] [CTTGCC]CT	1854 15016
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AAGTCACCTA TTCAATTAGG GCGAACCTGT GGGGTAA[GAA] GAGTCACCTA TTCAATTAGG GCGAT[ACAT] GGGGT[DATA]	1800 15056
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	[TTAA][T-]GG CGAGAACAC AC[GCGAAA TTAAAAAAA CTTAATCAGG CAGGAACCAT GTGACGAAA TTAAAAAAA	1933 15096
ISU 12/7q/3' terminal (1775 – 1938) Leijstad seq (14975 – 15101)	AAAAA AAAAA	1938 15101

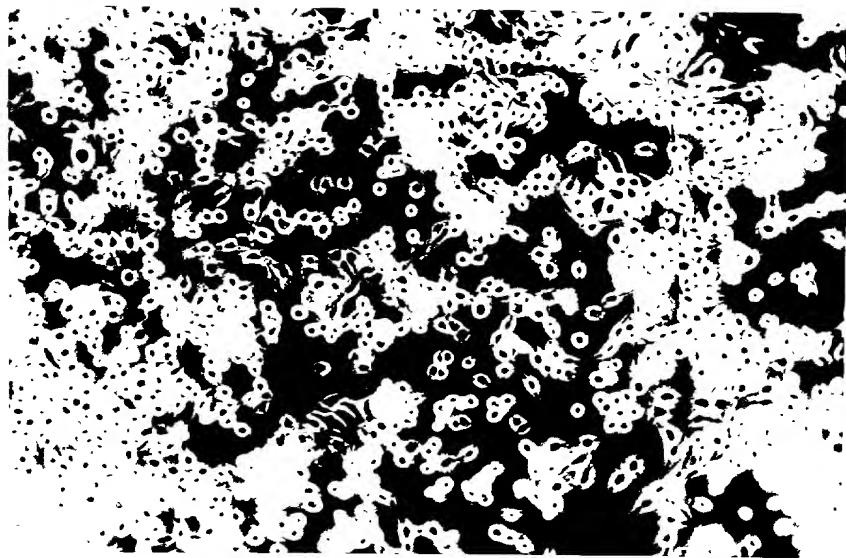
FIG. 11



**FIG.12**



**FIG.13**



**FIG.14**

SM E M NP E+M+NP SM

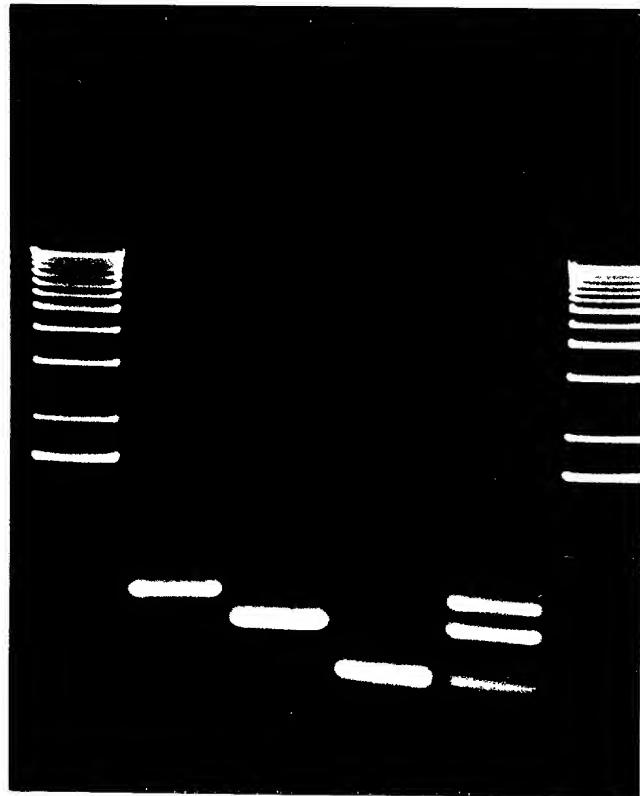


FIG.15

SM pVL1393 E M NP SM



FIG.16

John Smith, Virginia, 1607-1626; John Rolfe, Virginia, 1610-1675.

FIG. 17B

FIG. 17C

VR 2385	CTTGGACC-CCTGTCAGATTCAAGTTACACTGGGAGTTAGTTGGCTTAAGGATCATACTTGCGGTGATCCGGTCAAGGATCACCC-	877
ISU-1894	.....	-
ISU-22	.....	-
ISU-79	.....	-
ISU-55	.....	-
ISU-3927	C, T, T, - A, TCCAGC, A, G, C, TTCAG, T, TGG, GGTTCG, A, T, T, T, A, T, G	877
LV	.....	-

FIG. 17D

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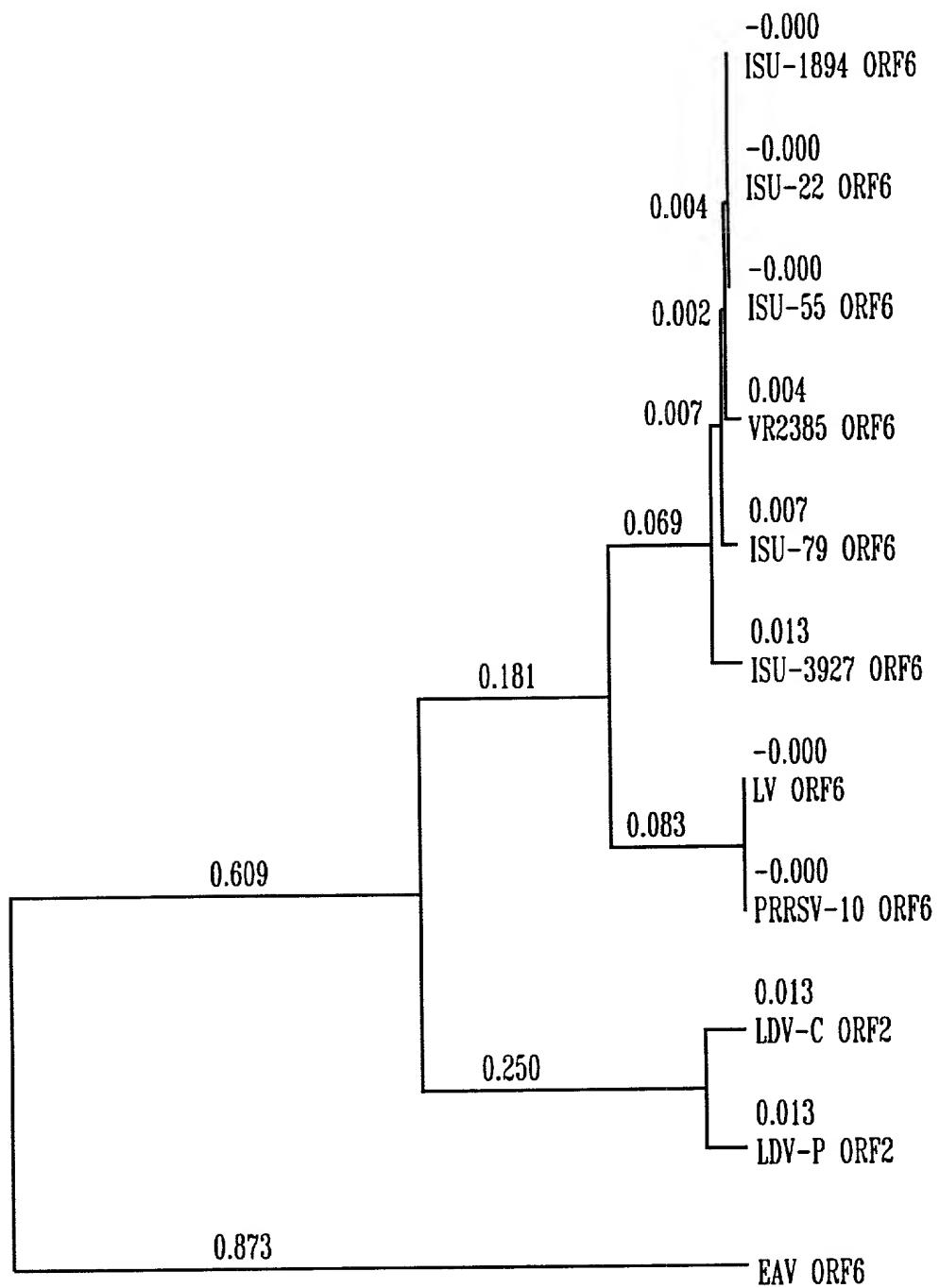
VR 2385	DRF6	LCLLGRKYILAPAHHVESAAAGFHPPIAANDNH-----AFVVVRPGSTTVNGTLVGGRKAVKQGWNLVKY-AK	183
ISU-1894	DRF6	-----	174
ISU-22	DRF6	-----	174
SIU-55	DRF6	-----	174
ISU-79	DRF6	-----	174
ISU-3927	DRF6	-----	174
LV	DRF6	C.....R.....L.....S.....SG.....R.....-----YA.....K.....L.....S.....R.....KR.....R.....	173
PRRSV-10	DRF6	C.....R.....L.....S.....SG.....R.....-----YA.....K.....L.....S.....R.....KR.....R.....	173
LDV-C	DRF2	F.....S.....PS.....D-----TSDGROSLLTTSLLT.....K.....L.....Q.....DFQR.....K.....SK.....A.....L.....VS.	171
LDV-P	DRF2	F.....S.....PS.....D-----TSDGROSLLTTSLLT.....K.....L.....Q.....DFQR.....K.....SK.....A.....L.....VS.	171

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W. H. Koch, Head  
W. H. Koch, Head  
W. H. Koch, Head

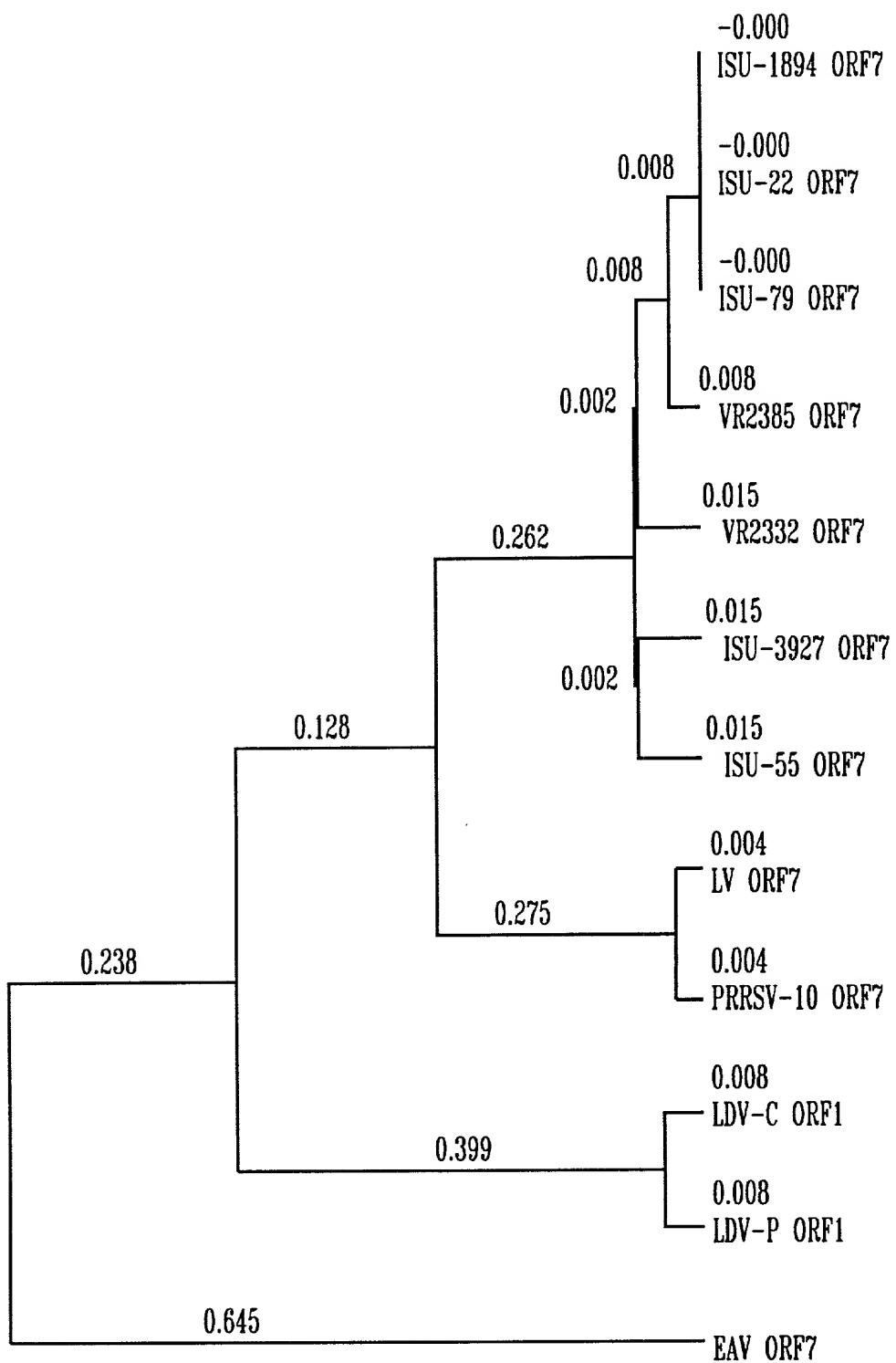
VR 2385	DRF7	MPNNTGKQQKKKK-----GDDQPVNQLCQMLGKIIAHQNQSRGKGPKKNNPEKPHFPLATEDDVRHHFTPSERQLCLSSIQTAFFNQGAGTCTLS	100
ISU-1894	DRF7	N.....	93
ISU-22	DRF7	N.....	93
ISU-79	DRF7	N.....	93
ISU-3927	DRF7	N.....K.....	93
ISU-55	DRF7	N.....K.....	93
VR2332	DRF7	N.....TEE.....	93
LV	DRF7	--A..N..SQ..KKSTAPM..N.....L..AM..KS..R----QPR..GQA..K.....A...I..L..QT..S..Q.....AS..	94
PRRSV-10	DRF7	--A..N..SQ..KKSTAPM..N.....L..AM..KS..R----QPR..GQA..K.....A...I..L..QT..S..Q.....PS..	94
LDV-C	DRF1	SQ..KK..GGQN..-----AN..-----N..LISALLRNAG..--N..K..Q..K..-Q..-L..M..GPS..L..VM..N..V..M..R..LV..L....G..Q...V	85
LDV-P	DRF1	SQ..KK..GGQN..-----AN..-----N..LINALLRNAG..--N..K..Q..K..-Q..-L..M..GPS..L..VM..N..V..M..R..LV..L....G..Q...V	85
EAV	DRF7	ASRRSRP..ASF-----RN..R--RRQPTSYNDLLRMFG..-----MRVR..PPAQOPTQAI..EPG..L..DLNGQ..ATLS..NV..RF..MI..H..SL..-A	83

VR 2385	DRF7	DSGRISYTVEFLPSTHHTVRLIRVTASP----SA	134
ISU-1894	DRF7	-----	123
ISU-22	DRF7	-----	123
ISU-79	DRF7	-----	123
ISU-3927	DRF7	P, -----	123
ISU-55	DRF7	-----	123
VR2332	DRF7	-----	123
LV	DRF7	S., KV, FQ, . M., VA, . . . . . STSASQGAS	128
PRRSV-10	DRF7	S., KV, FQ, . M., VA, . . . . . STSASQGAS	128
LDV-C	DRF1	G, NF, . S, M, . A, . . . . . NAS, NS-----	115
LDV-P	DRF1	G, NF, . S, M, . A, . . . . . NAS, NS-----	115
EAV	DRF7	A, GLT, . SW-V, . KQIQ, KVAPP, G, -----	110

FIG. 18B



*FIG. 19A*



*FIG. 19B*

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+ Start ORF2	CCTGAATTGAGATGAAATGGGGTCTATGCCAACCTTTTGACAAAATTGGCCAACCTTTTGATGGCTTACGGAGTTCTGGCATTTGTGAT	100
	ATCATATAATTGGCCATTGGTTGGCTCACCATCGCAAGGTTGCTATGAGGCCTTCTATGAGAAGATCCTATGAGGCCTTCTCTCAGTGGCAGATTGGTGGACATTCCCACCTGGAAACTAAACATCCCTTGGGGAA	200
	CTGGCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCTTCTATGAGGCTTCTCTCAGTGGCAGATTGGTGGAACTTGGAAACAGGTGGCTGGAAACAGGTGGCTGGAAACAGGT	300
	TGCTTTGGCACCATAGGGTCAACCCTAGTTGATGAAATGGTGTGAAATGGTGTGAAATGGTACGGCATCATGGAAAAAGCAGGACAGGGCTGGCTGGAAACAGGT	400
	AGTGAGGGAGGCATACGGCTGCTCGGATTAGTAGTTGGATGTGGATGGCTCAATTTCAGGATCTTGGCTGAGACCTGTAATATCTGGCC	500
	TCTCGGGTGGCATACACCACCTGGCATGACAAGGGTCAAATGTAACCATAGTGATAATAGTACTTTGAATCAGGTGTGTTGCTGTTTCCAAACCC	600
+ Start ORF3		
	GCTGTGGTTGGTTCCCATGGCTACGTACTGTTTGGTTGGCTGGCTGGTAACTTCTTCTGAACCTACGGTGAATTACACGGTGTGGCCGC	700
	CTTGGCTCACCGGGCAAGCAGCCACTTGGCATGGGATAGGGCATGATGAACTTCTTCTGACTCTTTGTGTGTTGAGCTATACGGCCAGTTC	800
	ACTAGGGTTGGTGGCCGCTGGCTTCCAGGAAAGGCCACTTGACAGTGCTTACGGCTGGCTCCCTGTCCTCAGGCTATACGGCCAGTTC	900
	CATCCCCGAGATACTGGGATAGGGAAATGGGAACTTGAGTGAGTGAGCTATGACATCAAGGACCAATTCTTGGCCTGTTCAAGCACCCTTGC	1000
		1100

FIG. 20A

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FIG. 20B

Consensus ATGMAATGGGTGCGMTGYRAGCCCTTTGAYAAAATYRGCCARCTKTTYGTTGAYGCYTTCACKGAGTTCYTKGTWSYRTKGTTGATA TRYAAATWTT 100  
VR2385 D<sub>R</sub>F2 ...A.....TA..CAA.....C....TG...A..T..T.....T..T.....G.....T..G..GTCCA..T.....CATT..A.. 100  
LV D<sub>R</sub>F2 ...C.....AC..TGG..-----T...CA...G..G..C....C..C....T..T.....G..T..TAGTG..G.....TGCC..T.. 91

Consensus YYTKGCCATWYTGTGGSTTACCCRITCGCAGGWTRSTGGTCCTTYKYMTCAGAKTGGTTTGCCTGGMWTCCGGTCKCGGCYCTGCCATTCAAC 200  
VR2385 D<sub>R</sub>F2 TT..G.....TT.....C.....A.....T.....C..GG.....T.....TGCA.....T.....A..A.....G.....C..... 200  
LV D<sub>R</sub>F2 CC..T.....AC.....G.....G.....A.....T.AC.....CTTC.....G.....C.T.....T.....T.....T..... 191

Consensus TCTSMSAAATYMGAAAGRCCATGARGSCCTTKYTSYCYMASITGMRSSYGGAYAKTCCCACAMTKGSARYYAARCAYCCWTTGGKATGYTTGGCA 300  
VR2385 D<sub>R</sub>F2 ...GAGC..T..CA...A.....G.C...TC..CT..TC..G...CAGGT..C..T.....-C..GG..G..ACT..A..T..T.....G..C..... 299  
LV D<sub>R</sub>F2 ...CCCC..C..TC...G.....A.G...GT..GC..CA..C...AGACC..T-G..A..TT..C..GTC..G..C..A.....T..T..... 290

Consensus CCATRMGAGTKTCCMMMCYTGGATTGARATGGTSTCKGTCGMAKTKACRSAYCATGGAAAMAWKCAAGGCARGCKGCCCTGGAARCAAGGTRGTKRGYGA 400  
VR2385 D<sub>R</sub>F2 ...AA..-..G..AAC..C.....A.....G..G.....A..G..GC..T.....A..AG..A..G..T.....A..A..GA..C.. 398  
LV D<sub>R</sub>F2 ...-..GC...T..CCA..T.....G....C..T.....C..T.....AG..C.....C..TT...T..A..G.....G..T.G..T.. 389

Consensus GGCYAUCCGTSTCWCAGMAYWIGTCAGGKVTSGATRTRGTRKRCCTCATTTYCARGCAYCTKGARGCSGAKWCYTGYMRMTWTCRSCTCWCGRGC 500  
VR2385 D<sub>R</sub>F2 ...T.....G..T..C..TTA..-..-..TT..G..GG.....T..G..T.....CA..T..A..C..GA..C..TAAA..A..GGC..T..G.. 496  
LV D<sub>R</sub>F2 ...C...-..C..A..A..GCT.....GC..C..A..A..TA.....C..A..C..G.....AG..G..G..G..A..C..G.....CAG..A..A..A.. 487

5' >----> 3'  
 5' <----< 3'

Consensus	TSSYSATGCTAMAMMAYCTGYCAYGWYAGGGTCAAATGTRASSCMTASWGAYAAYASSYACKTTGRAYCRSGTGTKWGCTCRTYTTCCOMACSCCWGGTV	600
VR2385 ORF2	GCCCC.....C.CC.C...C...T.AC.....A.GT....T..T.GT...T...A.T.AG...T...TT...-G.T....A..C..T...T	595
LV ORF2	CGTG.....A.AA.T..-T..-C.TT--.-,-.....G.GC..CA...C..C.CC..G...G.C.GC..-,GA...A.C...C..G..A..A	580
Consensus	CSMGGCCMAAGYTKMMYGAATTCTMRRCATGGCTMAATGCTCYATWTTTCCTCTGKGCKWCWTCKKTAACYYTKTTTYRTWGTGCTKTG	700
VR2385 ORF2	CC...A...C.TCAT.....CAG.....A..AGC...A..TT.C..T..A.....T..AG.T...TG..TC..T.....G..	695
LV ORF2	GA...C...T.GACC.....AGA.....CAG...G..CG.T..C..T.....G..TT.A..GT..CT.G..CA.A.....T..	680
Consensus	GYTKCGRRTCCARYKCTACGYWMGTGTTGGTTCCRYTGGYMYRSGGCAAYWTCWTTGARCTSACGGTGA	776
VR2385 ORF2	T..G..GG...ATG...TAC.....GC...TTAGG.....TTTT..T.....A..C.....	771
LV ORF2	C..T..AA.....GCT.....CTA.....AT...CCCAC...CACA..A.....G..G.....	750

*FIG. 214. 1*

Consensus	ATGGCTMATMRSTGTRCAKCYTCYATWTTTCTCTGTKGCKWKCWTCTKKTACYTKTTYRTWGCTKTGGYTKCGRRTCCARYKCTACGTYWMTGTT	100
LV DRF3	.....C.....CAG.....G.....CG.....T.....C.....T.....G.....TT.....A.....GT.....CT.....G.....CA.....AA.....T.....C.....T.....GCT.....AA.....GCT.....CTA.....	100
VR2385 DRF3	.....A.....AGC.....A.....TT.....C.....T.....A.....T.....AG.....T.....TG.....T.....TC.....T.....G.....T.....G.....GG.....T.....G.....ATG.....TAC.....	100

Consensus	TTTGGTTCCRYTGGYMRSGGCAAYWWTGCTGARCTSACSRSTAAYTACACSRTRTCGMYGCCYGGYYACCMGKCAAUURGTGGLMRARI	200
LV DRF3	.....AT...CCCAC.....CACA..A.....G..CA..C..C.....CA..A.....AT...C..TTCT..A..T.....G.....CA..A..G..	200
VR2385 DRF3	.....GC...TTAGG....TTTT..T.....A..C..GG..G..T.....GG..G..CC...T..CCTC..C..G.....A..-..AG..G..C..	199

Consensus	ACGARCCGGYMGKWMCMTKGGCARRATAGGGATGAYMGRGTGRRGGAGSSRYGAYCATGATGARYTAGKKWWTGCSRTSCCGTCTCGSSYWCCKMCA	300
LV ORF3	-...G....TC. TAA. A. G....AA.....CA. G....A....GGT. C.....GT. -..TTAA.....CA. C....C. .GTA. GA. .	298
VP22385	...A.....CA. GTC. C.....GG.....TC. A....G....GAC. T.....AC. .GGT. ....-GG. G. ....T. .CCT. TC. .	298

Consensus	RCMATTACCAASCAYCARRTMGACGGGGCAATTGGTTTCAAYTRGAATGGSTGGGKCCMTCCTTTCYICYGGKYMAAYRIMICWGGGTTTC	600
LV DRF3	G, A.....C, C, AA, A.....C, TT, G,.....C, G, AC,.....T, C, C,.....GC, CA, A, A.....	595
VR22385 DRF3	A, C.....G, T, GG, C,.....T, CC, A,.....G, T, CT,.....C, T, T,.....TT, A, T,.....TG, C, T,.....	598
Consensus	TSAAGGCCGTTCGCCCTGYAAGCCMTGTTTCWSKWCGMRTCTWTCAGAYATYRAGACCAACACSSACCGCRGKGCAGGGTTTYYRKGTCTTCARGAACATCART	700
LV DRF3	G,.....T,.....C,.....TCGA, CA,.....A,.....T,.....TG,.....G,.....G, T,.....CATG,.....T,.....G,.....A,	695
VR22385 DRF3	C,.....C,.....A,.....AGTT, AG,.....T,.....C, CA,.....A,.....G, A, C,.....TGCT,.....C, A,.....G,	698
Consensus	TGYYTYMGRCMTCACGGSRWCTRGAGKCAWGAGRMRATTTCCTTCGSAAGTCGGCYCARTGCGGCGAGMSGGWYRGTACTCCCCAGTAGCATCAGGA	800
LV DRF3	..TT, CC, A, C,.....GGT, ..A,.....G, A, AAA,.....G,.....T, C, A, T, T, A, C, TCG, .....	795
VR22385 DRF3	..CC, TA, G, A, ..---, CAA, ..G, ..--T, T, GCG, -----, C, ....-G, T, ..G, C, ..C-, G, ATA, -----	765

Consensus	TAA	803
LV	DRF3	798
VR2385	DRF3	765

FIG. 21B.1

FIG. 21C

Consensus	PLGM, WH., VS, LIDEMVSRR, Y., ME., GQAQWQVV, EATL, ., S, LD, V, HFQHLAA, EA., C., L, SRL, ML., L., ., NV., ., YN, TL., V., ., 200
LV DRF2.	.... F., MR., H., ., ., I., QT., HS, ., ., ., G., ., TKL, G., I., T., ., ., ., V., DS, RF, S, ., V., KN, AV--G., SLQ., T., DR, ELI 188
VR2385 DRF2.	.... L., HK., T., M., RI., KA., ., ., ., S., SRI, S., V, A., ., I., ET, KY, A., P., HH, RMTGS., TIV., S., NO, FAV 193

Consensus	FPTPG, RPKL, DF, QWLI, VH, SIFSSVA, S, TLF, VLWLR, P, LR, VFGF, W, A, . . . . .	264
LV DRF2,	. . . . . T, . . . . . T, . . . . . R, . . . . . S, . . . . . A, . . . . . S, V, . . . . . I, . . . . . I, A, Y, . . . . . H, PT, ---THSS	249
VR2385 DRF2	. . . . . S, . . . . . S, . . . . . H, . . . . . Q, . . . . . A, . . . . . S, . . . . . A, C, . . . . . V, . . . . . V, M, . . . . . T, . . . . . R, LG, IFLSNSR-	257

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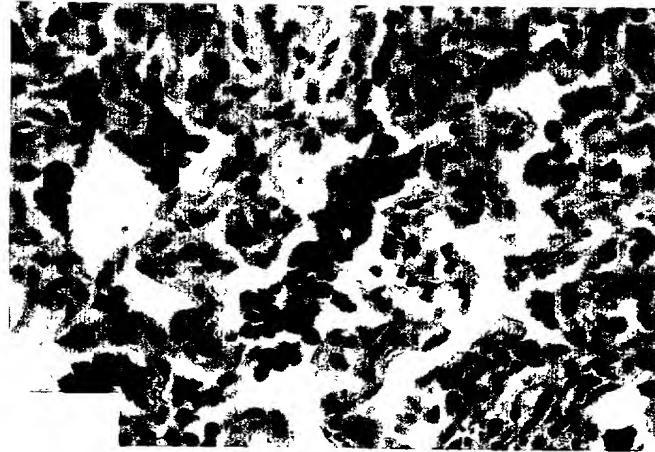
Consensus	MA., C., . . . FLC., . . . Y., . . . A., . . . S., . . . T., CFWFPL., GN, SFELT, NYT, C, PC, T, QAA, . . . EPGR, WC, TGHDRC, E, DHDEL, . . . PSG, . . . HQ, ARFHf, . . . GFIC, LVHS, LASN, SS, L, . . . AH, T, . . . I., I.M., S, S, . . . RQRl, . . . NM, K, . . . E, R, . . . LMSI, . . . YDN	100
LV DRF3.	NS, TFLYI, . . . CSFL, SFCC, VWAG, NA, Y	100
VRR2385 DRF3.	VR, F, . . . V, V.P., L, R, . . . AEAY, . . . SL, R, . . . G, D, . . . GFW, . . . LSS	100

Consensus	...L...YAWLA.LSFSY.AQFHPE.FGIGNVSRV.VD.HQFICA.HDG.N.I....NISA...YY.HQ.DGNNWFHLEW.RP.FSSWALVN.SWFL	200
LV DRF3,	L-K.EGY,...,F,...,A,...,L,...,F,...,KR,...,E,...,H,...,S,VSTGH,...,LYAA,...,H,...,I,...,L,...,L,...,I,...	199
VRR2385 DRF3,	EGH.TSA,...,S,...,T,...,I,...,Y,...,IK,...,V,...,Q,...,T,...,LPHHD,...,VLQT...,Q,...,V,...,V,...,V,...,V,...	200

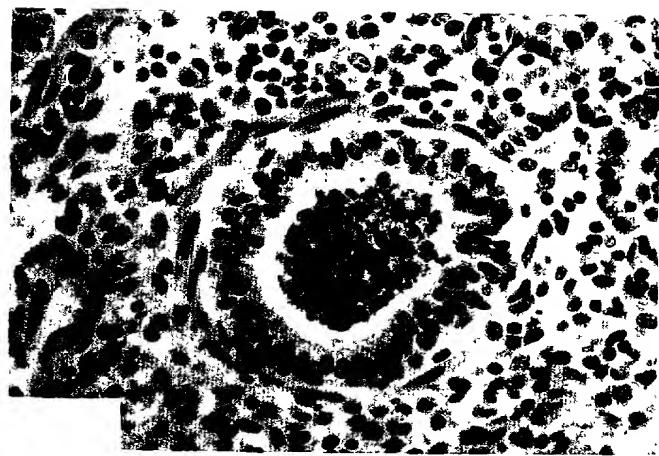
Consensus RRSP, S, VS, R, Q, RPT, P, . . . . . S, . . . TS, . . . L, . . . . . R, F, . . . . . K, S, . . . . .  
LV DRF3, . . . V, P, . . . R, IY, IL, . . . R, RLPVSW, FR, . . IVSD, TGQQRK, K, PSESRPNW, P, VLPTSR  
VBF22385 BE3 . . . AH, V, VE, TS, . . . P, QRSQAH, L, SK, . . V--A, GIAIRPL, R, A-----, LSARR-

FIG. 22B

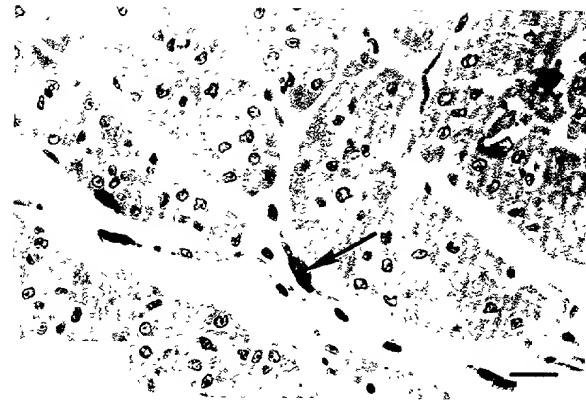
Consensus	M. A. LF. L. G. . . . . VS. AFACKPCFS. LSDI. TNTTAAAGF. VLQDI. C. R. . . . . A. E. I. . . K. QCR. A. GTP. YIT. TANVTD. YL. . . . DL	100
LV DRF4.	. A. AT. . F. A. AQHIM. E. . . . . TH. . . . . E. . . . . M. . . . . N. F. PHGVSA. Q. K. SFG. SS. . . E. V. . . Q. . . I. . . . . S. . . YNA. .	100
YD2205 RDE1	A S   HR--NS S.A. R-- VP. . . . . V. . . . . V. . . . . HSS. .	96



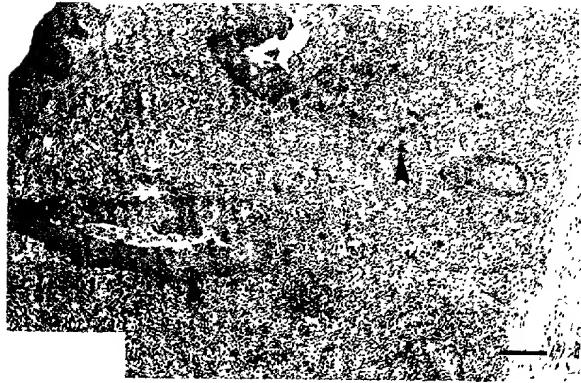
**FIG.23**



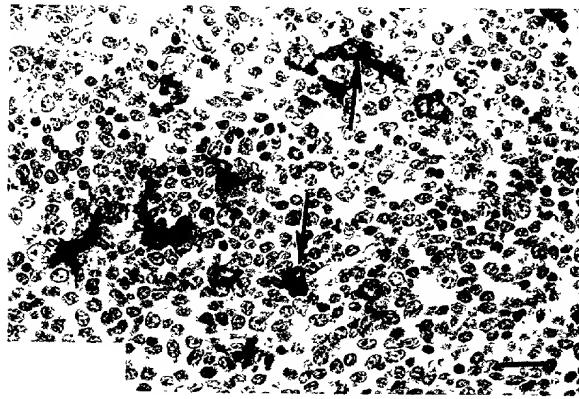
**FIG.24**



**FIG.25**



**FIG.26**



**FIG.27**



FIG. 28A



FIG. 28B



FIG. 28C

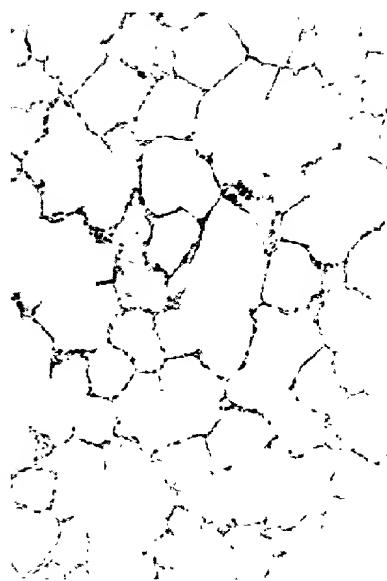


FIG. 29A



FIG. 29B

FIG. 29C

FIG.30A

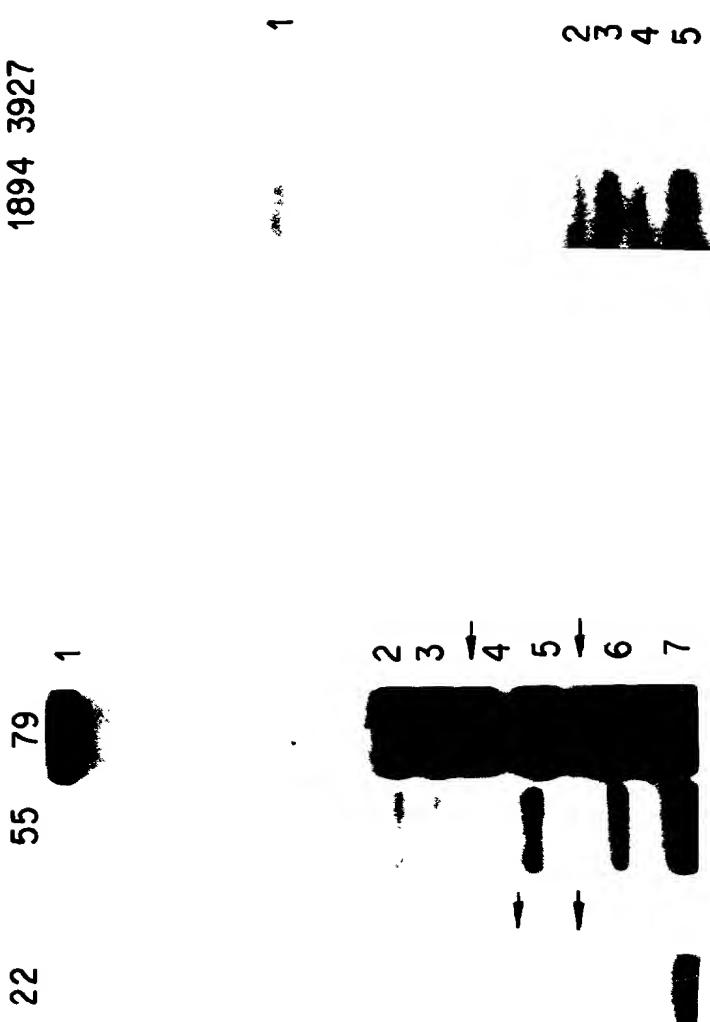


FIG.30B

